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APR 01 2003



1600

TECH CENTER 1600/2900

Does Not Comply
Correction Note Needed

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/033,742

DATE: 03/27/2003

TIME: 12:44:41

Input Set : A:\isph-623seq.txt

Output Set: N:\CRF4\03272003\J033742.raw

4 <110> APPLICANT: James Karras
 5 Thomas Condon
 7 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF MACROPHAGE INFLAMMATORY PROTEIN 3-
 ALPHA EXPRESSION
 9 <130> FILE REFERENCE: ISPH-0623
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/033,742
 C--> 11 <141> CURRENT FILING DATE: 2001-12-28
 11 <160> NUMBER OF SEQ ID NOS: 32

ERRORED SEQUENCES

389 <210> SEQ ID NO: 32
 390 <211> LENGTH: 20
 391 <212> TYPE: DNA
 392 <213> ORGANISM: Artificial Sequence
 394 <220> FEATURE:
 395 <221> NAME/KEY: unsure
 396 <222> LOCATION: (1-20)
 397 <223> OTHER INFORMATION: Antisense Oligonucleotide
 399 <400> SEQUENCE: 32
 W--> 400 nnnnnnnnnnnn nnnnnnnnnnn
 E--> 404 7

delete

ns in sequence,
 feature required.
 See enc summary sheet
 item 9

20

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/033,742

DATE: 03/27/2003

TIME: 12:44:42

Input Set : A:\isph-623seq.txt

Output Set: N:\CRF4\03272003\J033742.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:400 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32 after pos.:0
L:404 M:254 E: No. of Bases conflict, this line has no nucleotides.

Raw Sequence Listing Error Summary

1600

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 101033,742

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.